

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:
Rockey and Bannantine

Art Unit: Not yet assigned

Application No. Not yet assigned

CERTIFICATE OF MAILING

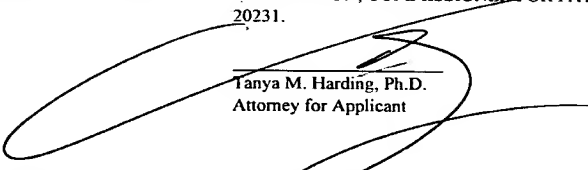
Filed: Herewith

I hereby certify that this paper and the documents referred to as being attached or enclosed herewith are being deposited with the United States Postal Service on October 16, 2000 in an Express Mail envelope addressed to: BOX PATENT APPLICATION, COMMISSIONER FOR PATENTS, WASHINGTON D.C. 20231.

For: CHLAMYDIA PROTEINS AND THEIR
USES

Examiner: Not yet assigned

Date: October 16, 2000


Tanya M. Harding, Ph.D.
Attorney for Applicant

STATEMENT IN COMPLIANCE WITH 37 C.F.R. § 1.821(f)

BOX PATENT APPLICATION
TO THE COMMISSIONER FOR PATENTS
Washington, DC 20231

Sir:

In compliance with 37 C.F.R. § 1.821(f), the undersigned declares that the sequence information recorded in computer readable form is identical to the written "Sequence Listing" provided herewith. No new matter has been added.

Respectfully submitted,

KLARQUIST SPARKMAN CAMPBELL
LEIGH & WHINSTON, LLP

By 

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PCT09

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/673,763

DATE: 01/18/2001
 TIME: 10:34:38

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3 <110> APPLICANT: Oregon State University
 5 <120> TITLE OF INVENTION: Methods of use for infection-specific INCA, INCB, and
 6 INCC proteins of Chlamydia
 8 <130> FILE REFERENCE: 52297
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/673,763
 C--> 11 <141> CURRENT FILING DATE: 2000-10-16
 13 <150> PRIOR APPLICATION NUMBER: 60/082,588
 14 <151> PRIOR FILING DATE: 1998-04-21
 16 <150> PRIOR APPLICATION NUMBER: 60/082,438
 17 <151> PRIOR FILING DATE: 1998-04-20
 19 <150> PRIOR APPLICATION NUMBER: 60/086,450
 20 <151> PRIOR FILING DATE: 1998-05-22
 22 <160> NUMBER OF SEQ ID NOS: 24
 24 <170> SOFTWARE: PatentIn Ver. 2.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 534
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Chlamydia trachomatis
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 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (1)..(534)
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 38 1 5 10 15
 40 aca ttt gca gct aat tct tca ggc aca att gga atc gtt aat tta cgt 96
 41 Thr Phe Ala Ala Asn Ser Thr Gly Thr Ile Gly Ile Val Asn Leu Arg
 42 20 25 30
 44 cgc tgc cta gaa gag tct gct ctt ggg aaa aaa gaa tct gct gaa ttc 144
 45 Arg Cys Leu Glu Glu Ser Ala Leu Gly Lys Lys Glu Ser Ala Glu Phe
 46 35 40 45
 48 gaa aag atg aaa aac caa ttc tct aac agc atg ggg aag atg gag gaa 192
 49 Glu Lys Met Lys Asn Gln Phe Ser Asn Ser Met Gly Lys Met Glu Glu
 50 50 55 60
 52 gaa ctg tct tct atc tat tcc aag ctc caa gac gac gat tac atg gaa 240
 53 Glu Leu Ser Ser Ile Tyr Ser Lys Leu Gln Asp Asp Asp Tyr Met Glu
 54 65 70 75 80
 56 ggt cta tcc gag acc gca gct gcc gaa tta aga aaa aaa ttc gaa gat 288
 57 Gly Leu Ser Glu Thr Ala Ala Ala Glu Leu Arg Lys Lys Phe Glu Asp
 58 85 90 95
 60 cta tct gca gaa tac aac aca gct caa ggg cag tat tac caa ata tta 336
 61 Leu Ser Ala Glu Tyr Asn Thr Ala Gln Gly Gln Tyr Tyr Gln Ile Leu
 62 100 105 110
 64 aac caa agt aat ttc aag cgc atg caa aag att atg gaa gaa gtg aaa 384
 65 Asn Gln Ser Asn Phe Lys Arg Met Gln Lys Ile Met Glu Glu Val Lys
 66 115 120 125
 68 aaa gct tct gaa act gtg cgt att caa gaa ggc ttg tca gtc ctt ctt 432

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69 Lys Ala Ser Glu Thr Val Arg Ile Gln Glu Gly Leu Ser Val Leu Leu
70      130      135      140
72 aac gaa gat att gtc tta tct atc gat agt tcg gca gat aaa acc gat 480
73 Asn Glu Asp Ile Val Leu Ser Ile Asp Ser Ser Ala Asp Lys Thr Asp
74 145      150      155      160
76 gct gtt att aaa gtt ctt gat gtt ctt ttc aaa ata att aac atg cga 528
77 Ala Val Ile Lys Val Leu Asp Val Leu Phe Lys Ile Ile Asn Met Arg
78      165      170      175
80 agc tag 534
81 Ser
84 <210> SEQ ID NO: 2
85 <211> LENGTH: 177
86 <212> TYPE: PRT
87 <213> ORGANISM: Chlamydia trachomatis
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91 1 5 10 15
93 Thr Phe Ala Ala Asn Ser Thr Gly Thr Ile Gly Ile Val Asn Leu Arg
94      20      25      30
96 Arg Cys Leu Glu Glu Ser Ala Leu Gly Lys Lys Glu Ser Ala Glu Phe
97      35      40      45
99 Glu Lys Met Lys Asn Gln Phe Ser Asn Ser Met Gly Lys Met Glu Glu
100      50      55      60
102 Glu Leu Ser Ser Ile Tyr Ser Lys Leu Gln Asp Asp Asp Tyr Met Glu
103 65 70 75 80
105 Gly Leu Ser Glu Thr Ala Ala Ala Glu Leu Arg Lys Lys Phe Glu Asp
106      85      90      95
108 Leu Ser Ala Glu Tyr Asn Thr Ala Gln Gly Gln Tyr Tyr Gln Ile Leu
109      100      105      110
111 Asn Gln Ser Asn Phe Lys Arg Met Gln Lys Ile Met Glu Glu Val Lys
112      115      120      125
114 Lys Ala Ser Glu Thr Val Arg Ile Gln Glu Gly Leu Ser Val Leu Leu
115      130      135      140
117 Asn Glu Asp Ile Val Leu Ser Ile Asp Ser Ser Ala Asp Lys Thr Asp
118 145 150 155 160
120 Ala Val Ile Lys Val Leu Asp Val Leu Phe Lys Ile Ile Asn Met Arg
121      165      170      175
123 Ser
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127 <211> LENGTH: 846
128 <212> TYPE: DNA
129 <213> ORGANISM: Chlamydia trachomatis
131 <220> FEATURE:
132 <221> NAME/KEY: CDS
133 <222> LOCATION: (1)..(846)
135 <400> SEQUENCE: 3
136 atg aat cgc atg att tgt gat tgc gtg tct cgc ata act ggg gat cga 48
137 Met Asn Arg Met Ile Cys Asp Cys Val Ser Arg Ile Thr Gly Asp Arg
138 1 5 10 15

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140 gtc aag aat att gtt ctg att gat gga gcg att gat cct cat tca tat 96
141 Val Lys Asn Ile Val,Leu Ile Asp Gly Ala Ile Asp Pro His Ser Tyr
142 20 25 30
144 gag atg gtg aag ggg gat gaa gac cga atg gct atg agc cag ctg att 144
145 Glu Met Val Lys Gly Asp Glu Asp Arg Met Ala Met Ser Gln Leu Ile
146 35 40 45
148 ttt tgc aat ggt tta ggt tta gag cat tca gct agt tta cgt aaa cat 192
149 Phe Cys Asn Gly Leu Gly Leu Glu His Ser Ala Ser Leu Arg Lys His
150 50 55 60
152 cta gag ggt aac cca aaa gtc gtt gat tta ggt caa cgt ttg ctt aac 240
153 Leu Glu Gly Asn Pro Lys Val Val Asp Leu Gly Gln Arg Leu Leu Asn
154 65 70 75 80
156 aaa aac tgt ttt gat ctt ctg agt gaa gaa gga ttc cct gac cca cat 288
157 Lys Asn Cys Phe Asp Leu Ser Glu Glu Gly Phe Pro Asp Pro His
158 85 90 95
160 att tgg acg gat atg aga gta tgg ggt gct gct gta aaa gag atg gct 336
161 Ile Trp Thr Asp Met Arg Val Trp Gly Ala Ala Val Lys Glu Met Ala
162 100 105 110
164 gcg gca tta att caa caa ttt cct caa tat gaa gaa gat ttt caa aag 384
165 Ala Ala Leu Ile Gln Gln Phe Pro Gln Tyr Glu Glu Asp Phe Gln Lys
166 115 120 125
168 aat gcg gat cag atc tta tca gag atg gag gaa ctt gat cgt tgg gca 432
169 Asn Ala Asp Gln Ile Leu Ser Glu Met Glu Glu Leu Asp Arg Trp Ala
170 130 135 140
172 gtg cgt tct ctc tct acg att cct gaa aaa aat cgc tat tta gtc aca 480
173 Val Arg Ser Leu Ser Thr Ile Pro Glu Lys Asn Arg Tyr Leu Val Thr
174 145 150 155 160
176 ggc cac aat gcg ttc agt tac ttt act cgt cgg tat cta tcc tct gat 528
177 Gly His Asn Ala Phe Ser Tyr Phe Thr Arg Arg Tyr Leu Ser Ser Asp
178 165 170 175
180 gcg gag aga gtg tct ggg gaa tgg aga tgg cgt tgc att tct cca gaa 576
181 Ala Glu Arg Val Ser Gly Glu Trp Arg Ser Arg Cys Ile Ser Pro Glu
182 180 185 190
184 ggg ttg tct cct gag gct cag att agt atc cga gat att atg cgt gta 624
185 Gly Leu Ser Pro Glu Ala Gln ile Ser ile Arg Asp ile Met Arg Val
186 195 200 205
188 gtg gag tat atc tct gca aac gat gta gaa gtt gtc ttt tta gag gat 672
189 Val Glu Tyr Ile Ser Ala Asn Asp Val Glu Val Val Phe Leu Glu Asp
190 210 215 220
192 acg tta aat caa gat gct ttg aga aag att gtt tct tgc tct aag agc 720
193 Thr Leu Asn Gln Asp Ala Leu Arg Lys Ile Val Ser Cys Ser Lys Ser
194 225 230 235 240
196 gga caa aag att cgt ctc gct aag tct cct tta tat agc gat aat gtc 768
197 Gly Gln Lys Ile Arg Leu Ala Lys Ser Pro Leu Tyr Ser Asp Asn Val
198 245 250 255
200 tgt gat aac tat ttt agc acg ttc cag cac aat gtt cgc aca att aca 816
201 Cys Asp Asn Tyr Phe Ser Thr Phe Gln His Asn Val Arg Thr Ile Thr
202 260 265 270
204 gaa gaa ttg gga ggg act gtt ctt gaa tag 846

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205 Glu Glu Leu Gly Gly Thr Val Leu Glu
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210 <211> LENGTH: 281
211 <212> TYPE: PRT
212 <213> ORGANISM: Chlamydia trachomatis
214 <400> SEQUENCE: 4
215 Met Asn Arg Met Ile Cys Asp Cys Val Ser Arg Ile Thr Gly Asp Arg
216 1      5      10      15
218 Val Lys Asn Ile Val Leu Ile Asp Gly Ala Ile Asp Pro His Ser Tyr
219      20      25      30
221 Glu Met Val Lys Gly Asp Glu Asp Arg Met Ala Met Ser Gln Leu Ile
222      35      40      45
224 Phe Cys Asn Gly Leu Gly Leu Glu His Ser Ala Ser Leu Arg Lys His
225      50      55      60
227 Leu Glu Gly Asn Pro Lys Val Val Asp Leu Gly Gln Arg Leu Leu Asn
228 65      70      75      80
230 Lys Asn Cys Phe Asp Leu Leu Ser Glu Glu Gly Phe Pro Asp Pro His
231      85      90      95
233 Ile Trp Thr Asp Met Arg Val Trp Gly Ala Ala Val Lys Glu Met Ala
234      100      105      110
236 Ala Ala Leu Ile Gln Gln Phe Pro Gln Tyr Glu Glu Asp Phe Gln Lys
237      115      120      125
239 Asn Ala Asp Gln Ile Leu Ser Glu Met Glu Glu Leu Asp Arg Trp Ala
240      130      135      140
242 Val Arg Ser Leu Ser Thr Ile Pro Glu Lys Asn Arg Tyr Leu Val Thr
243 145      150      155      160
245 Gly His Asn Ala Phe Ser Tyr Phe Thr Arg Arg Tyr Leu Ser Ser Asp
246      165      170      175
248 Ala Glu Arg Val Ser Gly Glu Trp Arg Ser Arg Cys Ile Ser Pro Glu
249      180      185      190
251 Gly Leu Ser Pro Glu Ala Gln Ile Ser Ile Arg Asp Ile Met Arg Val
252      195      200      205
254 Val Glu Tyr Ile Ser Ala Asn Asp Val Glu Val Val Phe Leu Glu Asp
255      210      215      220
257 Thr Leu Asn Gln Asp Ala Leu Arg Lys Ile Val Ser Cys Ser Lys Ser
258 225      230      235      240
260 Gly Gln Lys Ile Arg Leu Ala Lys Ser Pro Leu Tyr Ser Asp Asn Val
261      245      250      255
263 Cys Asp Asn Tyr Phe Ser Thr Phe Gln His Asn Val Arg Thr Ile Thr
264      260      265      270
266 Glu Glu Leu Gly Gly Thr Val Leu Glu
267      275      280
270 <210> SEQ ID NO: 5
271 <211> LENGTH: 361
272 <212> TYPE: DNA
273 <213> ORGANISM: Chlamydia trachomatis
275 <220> FEATURE:
276 <221> NAME/KEY: CDS

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282 1 5 10 15
284 tta cag aag aat tgg gag gga ctg ttc ttg aat aga gat aat gca att 96
285 Leu Gln Lys Asn Trp Glu Gly Leu Phe Leu Asn Arg Asp Asn Ala Ile
286 20 25 30
288 gct tgg tcc gta gag gat ctt tgt gtt aat tat gat cac tca gac gtc 144
289 Ala Trp Ser Val Glu Asp Leu Cys Val Asn Tyr Asp His Ser Asp Val
290 35 40 45
292 tta tgt cac att act ttt tct ctg cct gca ggg gca atg gct gct att 192
293 Leu Cys His Ile Thr Phe Ser Leu Pro Ala Gly Ala Met Ala Ala Ile
294 50 55 60
296 att ggg ccg aat gga gct ggt aaa agt act ttg ctt aag gct tct tta 240
297 Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Lys Ala Ser Leu
298 65 70 75 80
300 gga ctg att cgt gct tct tct ggc caa agc ttg ttc ttt ggt cag aga 288
301 Gly Leu Ile Arg Ala Ser Ser Gly Gln Ser Leu Phe Phe Gly Gln Arg
302 85 90 95
304 ttt tcc aag gca cat cat aga ata gcc tat atg cct caa aga gcg agt 336
305 Phe Ser Lys Ala His His Arg Ile Ala Tyr Met Pro Gln Arg Ala Ser
306 100 105 110
308 gtg gat tgg gat ttc cca atg act gtt ctt gat ctc gtg ttg atg ggg 384
309 Val Asp Trp Asp Phe Pro Met Thr Val Leu Asp Leu Val Leu Met Gly
310 115 120 125
312 tgt tac ggc tat aaa gga ata tgg aat cgt att tcc act gat gat cgt 432
313 Cys Tyr Gly Tyr Lys Gly Ile Trp Asn Arg Ile Ser Thr Asp Asp Arg
314 130 135 140
316 cag gag gct atg cgt att tta gag cgg gtt ggt ttg gaa gct ttt gca 480
317 Gln Glu Ala Met Arg Ile Leu Glu Arg Val Gly Leu Glu Ala Phe Ala
318 145 150 155 160
320 aat cgt caa ata ggt aag ctc tct gga gga caa caa cag aga gct ttt 528
321 Asn Arg Gln Ile Gly Lys Leu Ser Gly Gly Gln Gln Gln Arg Ala Phe
322 165 170 175
324 tta gcg cgg tca tta atg caa aaa gca gat ttg tat ctc atg gat gag 576
325 Leu Ala Arg Ser Leu Met Gln Lys Ala Asp Leu Tyr Leu Met Asp Glu
326 180 185 190
328 ctg ttc tct gcg atc gat atg gcc tct tat cag atg gtt gta gat gtt 624
329 Leu Phe Ser Ala Ile Asp Met Ala Ser Tyr Gln Met Val Val Asp Val
330 195 200 205
332 ttg caa gag ctt aaa agc gaa ggg aag act att gtg gtc att cat cat 672
333 Leu Gln Glu Leu Lys Ser Glu Gly Lys Thr Ile Val Val Ile His His
334 210 215 220
336 gat ttg agt aat gtc cgg aag ctt ttt gat cat gtg att tta tta aat 720
337 Asp Leu Ser Asn Val Arg Lys Leu Phe Asp His Val Ile Leu Leu Asn
338 225 230 235 240
340 aag cat ctt gtg tgc tct gga agc gta gaa gaa tgc ttg act aaa gaa 768
341 Lys His Leu Val Cys Ser Gly Ser Val Glu Glu Cys Leu Thr Lys Glu

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